1. Background

Vancomycin resistant Enterococcus faecium (VREfm) was only detected sporadically in the Region of Southern Denmark until 2016, when a rise in number of cases appeared in the University Hospital. Multi Locus Sequence Typing (MLST) and core genome MLST (cg-MLST) based on Whole Genome Sequencing (WGS) were carried out in order to:
- trace transmission routes
- assess the two methods as epidemiological tools using sequence types (STs) and complex types (CTs)

2. Materials/methods

- One VREfm isolate from each of all 38 patients
- Period: January 2014 - June 2017
- WGS
- MLST and cg-MLST
- Cluster arrangement and phylogeny
- Epi-curves of ST and CT

3. Results

MLST:
- 6 different STs
- ST-80: 26 isolates

Cg-MLST:
- 19 different CTs
- ST-80: subdivided into 7 different CTs and 5 isolates with no assigned CT
- CT-993: dominated and consisted of 12 of the ST-80 isolates

Epi-curves:
- CT-993 was transmitted between 7 patients

4. Conclusion

- Cg-MLST
  - allowed a more detailed distinction between types than MLST
  - gave evidence of transmission of specific CTs
  - may prove to be a valuable tool in infection control
- Both MLST and cg-MLST should be supplemented with admission history in outbreak investigation

Figure 1. Neighbor Joining Tree based on MLST but colored by cg-MLST. The different colours in each cluster indicates a subdifferentiation if cg-MLST is used.

Figure 2. Epi-curves with the ST and CT of the isolates. Each isolate is in the same place in each of the schemes.